

FIG. |A-|

Signal pentide

MMP-1
MMP-2
MMP-3
MMP-7
MMP-8
MMP-9
MMP-10
MMP-11
MMP-12
MT-MMP-1
MT-MMP-3
consensus

MMP-1
MMP-2
MMP-3
MMP-7
MMP-8
MMP-9
MMP-10
MMP-11
MMP-12
T-MMP-1
T-T-MMP-3
consensus

Pro-peptide

DA ETI KVMMKOPRRCGV P DVAQ
DQNTIETMRKPRCGNPDVAN-----
DSDTLEVMRKPRCGVPDVGH-----
NSRVEIEMOKPRCGVPDVAE-----
NEETLDMMKKPRCGVPDSGG-----
DSATLKA MMRKPRCGVPDLGR-----
DQDTLEVMRKPRCGVPDVHG-----
APRPASSLRP RCGVPDP SD-GLSA RNQKRKFVLLSG
DTSTLEMMHAPRCGV P DLHH-----
DADTMKAMRRPRCGVPDKFGAEIKANVRKRYAI Q-G-LWQHNEIT
DORTIDWMK KPRCGVPDQTRGSSSKFHIRRKRYALTGQ-Q-WQKHIT
TL MAKPKPCCYVDD

IS-1

FIG. IA-2**Pro-peptide**

EQDVLDLVQKYLEKYYNLKNDGROPEKRRNNSGPVV-EKLIKOMQEFFFGLKVTKVGTGKP	79
DVAPK-TDKELAVQYLNTE-YGCPKE-SCNLFVULKDTLKKMOKFFGLGLEVTGKL	89
DTSMNLYVKYLFENYYDLKKDVKQFVRRKDSGPVV-KKIREM-QKFGLGLEVTGKL	79
AGGMSELQWEQADY-LKRFYLYLDSETKNANSLE-AKLEMEMOKFFGLPITGML	74
EKNTKTVQDYLEKFYQLPSNOYQSTR-KNGTINVIVEKLEMEMQREFFGLNVNTGKP	78
DLRTNTLTDRLQLAFFYLRYGYTRVAEMRGESKSLSGPALLLQQQLQLSPETGEL	86
DSNKDLAQQYLEKYYNLKEVDVKQFRRK-DSNLIV-KKIGCMQKFGLGLEVTGKL	78
-----PDVHHLHAERRGPO-----	67
KNNVLFGERYLEKFYGGLEINKLETRKMYKSGNIMKEK1QHFLGLKVTKVGTGQL	79
-----EAMLQQGYLPPGDLRHTTQRSPQSLS-AALIAQMOKFYGQLQVTGKA	80
TEQYFNIEWLQKRYGYLPPTSPRMWSVYRAETMO-SALAAMOOFYGINMTGKV	88
.....L....Y.L.....K.L.....KL..MQKF..GL..VTGKL	100

Catalytic

YRIENYTPDLPRADVDAHAIKEKAFQIWSNVTPLTFTKV-----SEGOADIM	160
YRIIGYTPDLDPETVDDAFAFARAFQWSDVTPLRSRI-----HDGEADIM	170
YRIVNYTPDLPKDAVIDSAVEKAALKWEEEVTPLTSR-----YEGEADIM	160
YRIVSYTYRDPLPHITVDRILSKA1NMWGKEIP1HFRKV-----VWGTADIM	155
YRIRNYTPQLSSEAVERAIKDAFELWSASPLIFTRI-----SQGEADIN	159
YWIONYSEDILPRAVIIIDAFARAFAFLWSAVTPLTFTRV-----YSRDADIV	167
YRIVNYTPDLPRDAVDSAIEKAALKWVVEEVTPLTSR-----YEGEADIM	159
YRILRFPWQLVQEQRVOTMAEAALKWWSDVTPLTFTEV-----HEGRADIM	156
YRINNYTPDMNRDVEDYAIRKAQFQVWSNVTPLFKFSKI-----NTGMADIM	160
FCIONYNTPKVGEYAYEAIKRAFQVWSATPLRFREVYPAYIREGHEKQADIM	178
YSIKNVTPKVGDPETRKAIRRAFDVWQNPVSELENG-KRDVDIP	185
YRI.NYTPDL...V.D..AI..KAF..VWS..VTPLTF..V...G..ADIM	200

FIG. B-1

Catalytic	
MMP-1	ISFVRGDHRDNSPFDGPGGNLAHAFAFPQGP GIGGDAHFDEHERWTN-NFTEYNN INFGRWEHGDDGYPFDGKDGILLAHAFAFPCTGVGGDSHFDDELWTLGEQQVWR ISFAVREHGDFYPFDGPGNVLAHAAYAPGP GINGDAHFDDDEOKTK-DTGTGN MMP-2
MMP-3	IGFARGAHGDSYSPFDGPGNTLAHAFAFPGTGLGDDAHF DEDERWTIDGSSLGIN MMP-7
MMP-8	IAFYQRDHGDNSSPFDGPNGILIAHAFAOPCQGIGGDAHFDAEWTWN-TSANYN MMP-9
MMP-10	IQFGVAHGDDGYPFDGKDGFHDQGDAHFDDDEILWSLGKGVVVP ISFAVKEHGDFYSFDGKDPGHSILAHAYAPP GP GLYGDIFH DDEKWTEDASGTN MMP-11
MMP-11	IDFARYWDGDDLPFDGPGGILAHAFAPPKTHREGDYFDYDTEWTIDGDDQTG VVFARGAHGDFHAFDGKGGILAHAFGP GSGIGGDAHF DDEFDEFWTN-HSGGDTN MMP-12
MT-MMP-1	IEFAEGFHGDSTPFDGEGGFLAHAYFP GP NIGGDTNFDSAEPWTW-RNEDLN MMP-12
MT-MMP-3	IIIFASGFHGDSSSPFDGEGGFLAHAYFP GP GIGGDTFIDSDEPWTLGNPNPHDGN I.FA...HGD..PPFDGPGG .LAHAF .PGP GIGGDAHF .DE.WT.-....N
Consensus	
Catalytic	
MMP-1	----- YGFCPHEALFTMGGNAEGQPKCFPRFQGTSYDSCTTEGRTDGYRWCGTTED
MMP-2	----- -----
MMP-3	----- -----
MMP-7	----- -----
MMP-8	----- -----
MMP-9	----- -----
MMP-10	----- -----
MMP-11	----- -----
MMP-12	----- -----
MT-MMP-1	----- -----
MT-MMP-3	----- -----
Consensus	

FIG. IB-2

FIG. IC-1

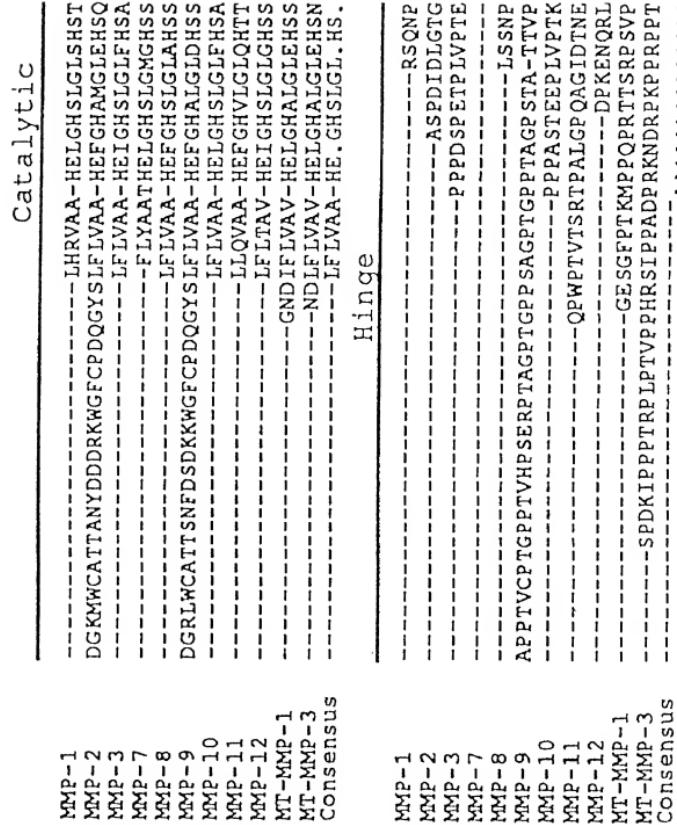


FIG. IC-2

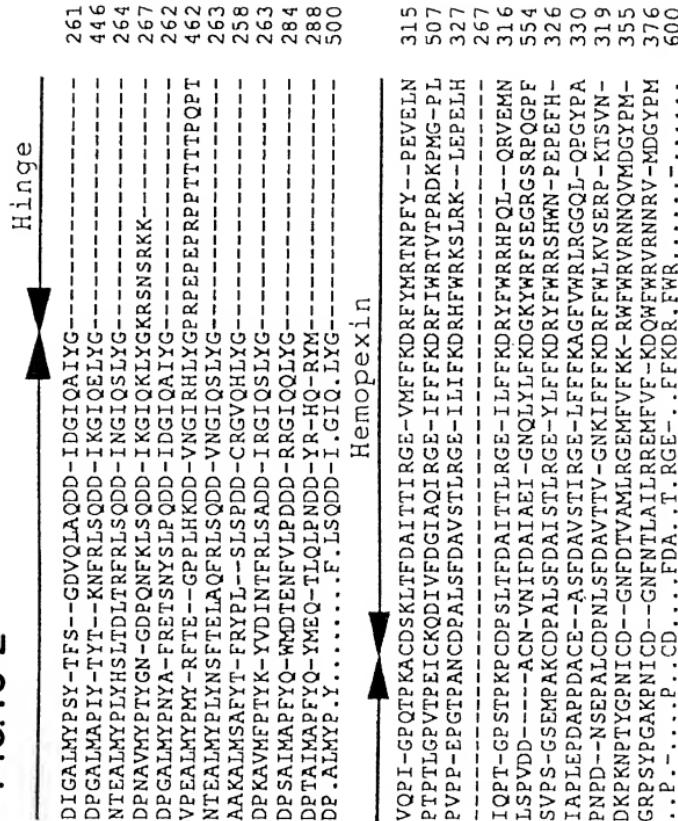


FIG. ID-1

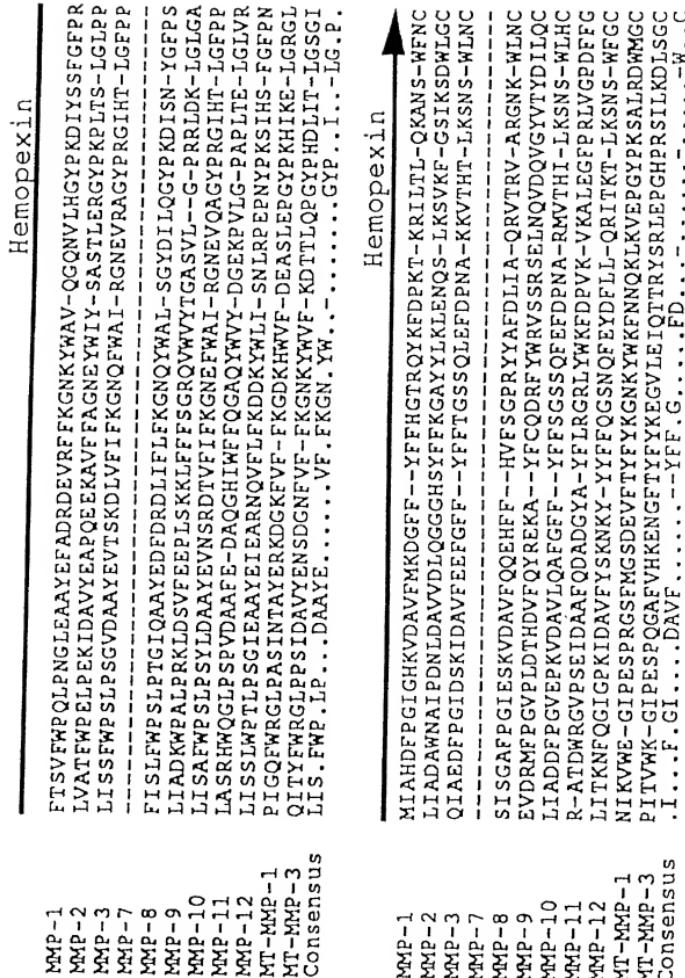


FIG. ID-2

TVKHIDAA-LSEENTGKTYFFVANKYWRYDEYKRSMDPGYPK	413
DVQRVDAA-FNWSKNKKTYIFAGDKFWRYNEVKKKMDPGFPK	604
TVRKIDAA-ISDKEKNKTYFPEVDKWRFDEKRNSMEPGFPK	424
SVOAIDAA-VFYRS---KUYFFFVNDQFWRYDNQROFMEPGYPK	267
DVAQVTGA-LRSGR-GKMILLESGRRLMREDFVKAQMVDPRSAS	411
TIRKIDAA-VSDKEKKKTYFFAADKTYWRFDENSQSMEQQGFPK	648
FP---VHAALVWGP-EKNKTYFFGRDYWRFRFHPSSTRRVDSVPR	423
FVKKIDAA-VFNPRFYRTYFFVDNOQWRYDERRQMDPGYPK	424
PTDKIDAA-LFWMPNGKTYFFRGNKYYRFNEELRAVIDSEVPK	416
PPHGIDS-A-IWEDVGKTYFFKGDRYWRYSEEMKTMDPGYPK	451
.V..IDAA-.....KTYFF.....YWR.DE....MDPG.PK	700
RKN-----	469
-----	660
-----	477
-----	267
RYG-----	467
PED-----	707
-----	476
CAEPANTFL-----	488
-----	470
PSGGRPDEGTEETE-VIIIEVDEEGGAVASAAYVLPVLL	549
DGPTDRVKEGHSPDDVDIVIKLDNTASTVKAIATIVPCILA	571
-----	800

FIG. 1E

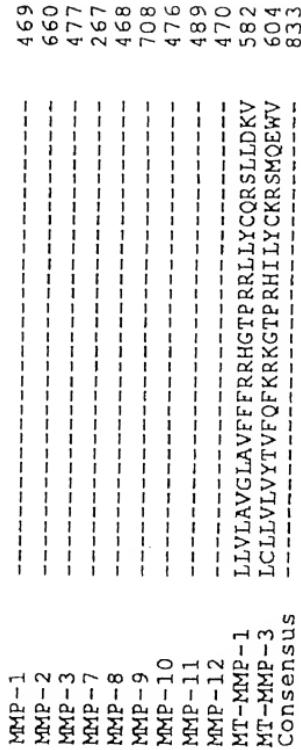


FIG. 2

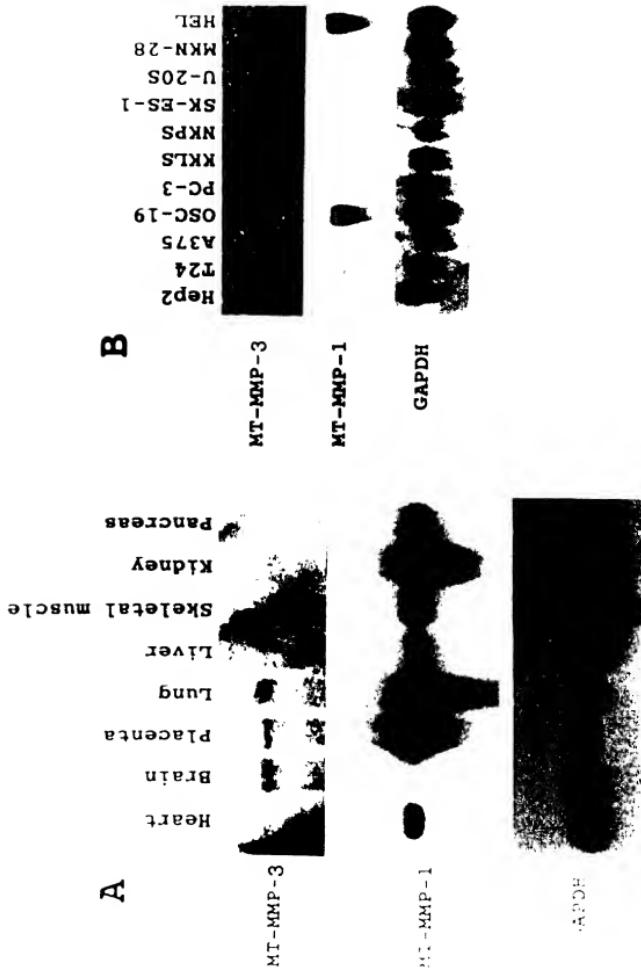


FIG. 3

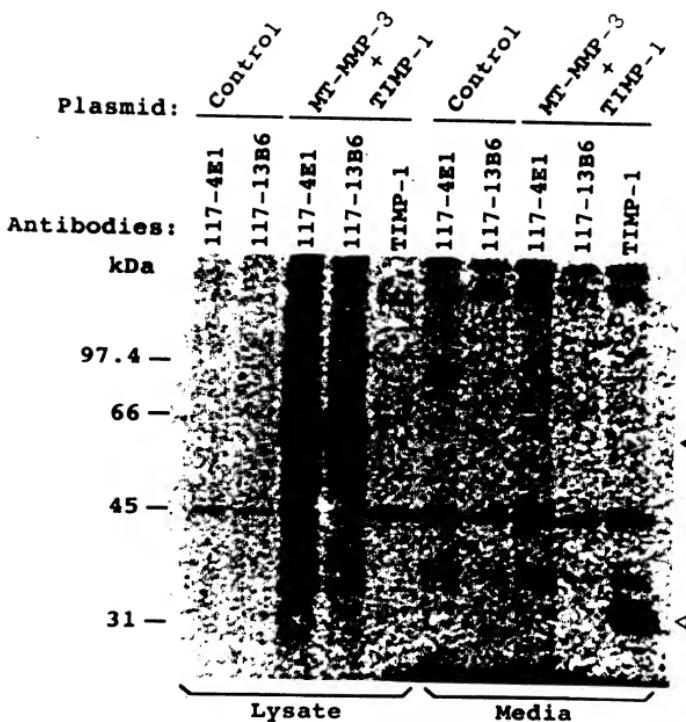
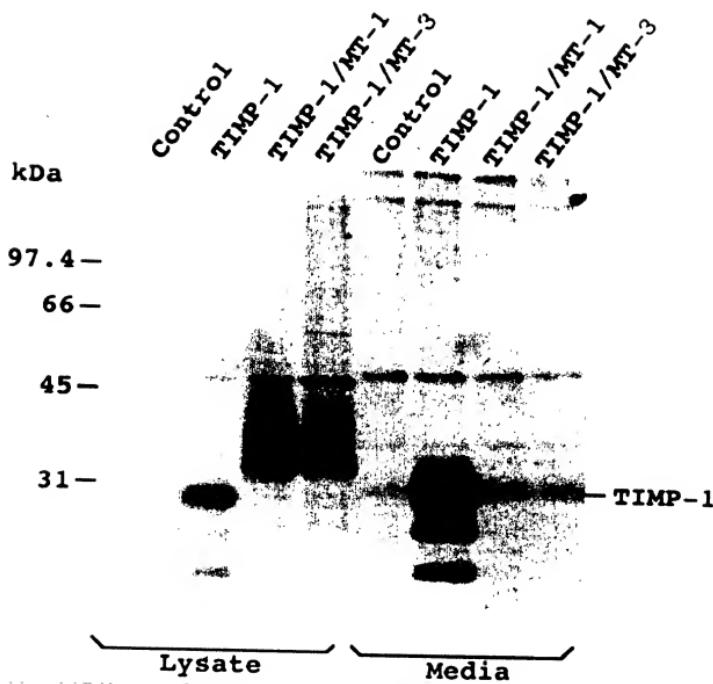


FIG. 4



09734002-121203



FIG. 5

09734002"121200

FIG. 6

